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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/035,060

DATE: 01/30/2002

TIME: 18:05:01

Input Set : N:\Crf3\RULE60\10035060.raw.txt

Output Set: N:\CRF3\01302002\J035060.raw

1 <110> APPLICANT: Edwards, David
2 Wong, Siu-Yin
3 Herrnstadt, Corinna
4 Wilcox, Edward
5 <120> TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
6 Toxicity Of
7 Bacillus Thuringiensis Lepidoteran Toxins, and Recombinant DNA Sequences
8 Therefor
9 <130> FILE REFERENCE: M12C1FDF3D1
10 <140> CURRENT APPLICATION NUMBER: 10/035,060
11 <141> CURRENT FILING DATE: 2001-12-27
13 <150> PRIOR APPLICATION NUMBER: 09/405,788
14 <151> PRIOR FILING DATE: 1999-09-27
17 <150> PRIOR APPLICATION NUMBER: US 08/580,781
18 <151> PRIOR FILING DATE: 1995-12-29
19 <150> PRIOR APPLICATION NUMBER: US 08/420,615
20 <151> PRIOR FILING DATE: 1995-04-10
21 <150> PRIOR APPLICATION NUMBER: US 08/097,808
22 <151> PRIOR FILING DATE: 1993-07-27
23 <150> PRIOR APPLICATION NUMBER: US 07/980,128
24 <151> PRIOR FILING DATE: 1992-11-23
25 <150> PRIOR APPLICATION NUMBER: US 07/803,920
26 <151> PRIOR FILING DATE: 1991-12-06
27 <150> PRIOR APPLICATION NUMBER: US 07/356,599
28 <151> PRIOR FILING DATE: 1989-05-24
29 <150> PRIOR APPLICATION NUMBER: US 06/904,572
30 <151> PRIOR FILING DATE: 1986-09-05
31 <150> PRIOR APPLICATION NUMBER: US 06/808,129
32 <151> PRIOR FILING DATE: 1985-12-12
33 <160> NUMBER OF SEQ ID NOS: 9
34 <170> SOFTWARE: PatentIn version 3.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 3537
38 <212> TYPE: DNA
39 <213> ORGANISM: Bacillus Thuringiensis
40 <400> SEQUENCE: 1
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43 tcgctaacgc aattttctttt gagtgaattt gttcccggtg ctggatttgt gttaggacta 180
44 gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttcc tgtacaaatt 240
45 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
46 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
47 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgc 420

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50	aggtggggat	ttgatgccgc	gactatcaat	agtcgttata	atgatttaac	taggcttatt	600
51	ggcaactata	cagattatgc	tgtgcgctgg	tacaatacgg	gattagagcg	tgtatgggga	660
52	ccggattcta	gagattgggt	aaggtataat	caatttagaa	gagagctaac	acttactgta	720
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56	aatagtataa	ccattttatac	tgatgtgcat	agaggcttta	attattggtc	agggcatcaa	960
57	ataacagctt	ctcctgtagg	gttttcagga	ccagaattcg	cattcccttt	atttggaat	1020
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75	gatgaacgca	atttactcca	agattcaaat	ttcaaagaca	ttaataggca	accagaacgt	2100
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79	caagacttag	aaatctattt	aattcgctac	aatgcaaaac	atgaaacagt	aaatgtgccca	2340
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91	gaagaacaaa	acaaccaacg	ttcggtcctt	gttggtccgg	aatgggaagc	agaagtgtca	3060
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93	ggatatggag	aagggttgct	aaccattcat	gagatcgaga	acaatacaga	cgaactgaag	3180
94	tttagcaact	gcgtagaaga	ggaaatctat	ccaaataaca	cggtaacgtg	taatgattat	3240
95	actgtaaate	aagaagaata	cggaggtgcg	tacattcttc	gtaatcgagg	atataacgaa	3300
96	gtccttcccg	taccagctga	ttatgcgtca	gtctatgaag	aaaaatcgta	tacagatgga	3360

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102 <211> LENGTH: 1177
103 <212> TYPE: PRT
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105 <400> SEQUENCE: 2
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109      20          25          30
110      Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
111      35          40          45
112      Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
113      50          55          60
114      Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
115      65          70          75          80
116      Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
117      85          90          95
118      Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
119      100         105         110
120      Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
121      115         120         125
122      Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
123      130         135         140
124      Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
125      145         150         155         160
126      Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
127      165         170         175
128      Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
129      180         185         190
130      Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
131      195         200         205
132      Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
133      210         215         220
134      Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
135      225         230         235         240
136      Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
137      245         250         255
138      Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
139      260         265         270
140      Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
141      275         280         285
142      Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
143      290         295         300
144      Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
145      305         310         315         320
146      Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro

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150	Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr
151				355				360				365	
152	Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser
153				370				375				380	
154	Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro
155				385				390			395		400
156	Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile
157					405					410			415
158	Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg
159				420						425			430
160	Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val
161				435				440					445
162	Arg	Ala	Pro	Thr	Phe	Ser	Trp	Gln	His	Arg	Ser	Ala	Glu
163				450				455				460	
164	Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr
165				465				470				475	480
166	Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly
167					485					490			495
168	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser
169				500						505			510
170	Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val
171				515						520			525
172	Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile
173				530						535			540
174	Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser
175				545						550			555
176	Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr
177					565					570			575
178	Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His
179				580						585			590
180	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val
181				595						600			605
182	Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln
183				610						615			620
184	Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys
185				625						630			635
186	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu
187					645					650			655
188	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Gln	Glu	Leu	Ser	Glu
189				660						665			670
190	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln
191				675						680			685
192	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg
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194	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu
195				705						710			715
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198 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
199 740 745 750
200 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
201 755 760 765
202 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
203 770 775 780
204 Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
205 785 790 795 800
206 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
207 805 810 815
208 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
209 820 825 830
210 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
211 835 840 845
212 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
213 850 855 860
214 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
215 865 870 875 880
216 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
217 885 890 895
218 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
219 900 905 910
220 Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
221 915 920 925
222 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
223 930 935 940
224 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
225 945 950 955 960
226 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
227 965 970 975
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229 980 985 990
230 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
231 995 1000 1005
232 Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
233 1010 1015 1020
234 Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
235 1025 1030 1035
236 Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
237 1040 1045 1050
238 Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
239 1055 1060 1065
240 Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
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242 Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
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244 Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys

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